OIPE JC42 DEC 10 2002 PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

<110> LITTLE, MELVYN
KIPRIYANOV, SERGEY
MOLDENHAUER, GERHARD
DEUTSCHES KREBSFORSCHUNGSZEUTRUM

<120> MUTATED OKT3 ANTIBODY

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<140> 09/424,705
<141> 2000-06-02

<150> PCT/DE98/01409
<151> 1998-05-22

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<213> Homo sapiens

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                                1               5

gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag      102
Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
 10                  15                  20                  25

ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag      150
Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
                 30                  35                  40

atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac      198
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
             45                  50                  55

tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att      246
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
         60                  65                  70

aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag      294
Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys
     75                  80                  85
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gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg caa ctg      342
Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
 90                  95                 100                 105

agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca aga tat      390
Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr
                110                 115                 120

tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc act ctc      438
Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu
            125                 130                 135

aca gtc tcc tca gcc aaa aca aca ccc aag ctt gaa gaa ggt gaa ttt      486
Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe
        140                 145                 150

tca gaa gca cgc gta gat atc gtg ctc act cag tct cca gca atc atg      534
Ser Glu Ala Arg Val Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met
    155                 160                 165

tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca      582
Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
170                 175                 180                 185

agt gta agt tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc      630
Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro
                190                 195                 200

aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct      678
Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
            205                 210                 215

cac ttc agg ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc      726
His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
        220                 225                 230

ggc atg gag gct gaa gat gct gcc act tat tac tgc cag cag tgg agt      774
Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
    235                 240                 245

agt aac cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg      822
Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg
250                 255                 260                 265

gct gat act gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa      870
Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu
                270                 275                 280

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Asp Leu Asn Ser His His His His His His
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<210> 2
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            20   25   30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35   40   45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50   55   60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65   70   75   80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
                85   90   95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
            100   105   110
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu
        115   120   125
Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
    130   135   140
Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Asp Ile
145   150   155   160
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
                165   170   175
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            180   185   190
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
        195   200   205
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
    210   215   220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
225   230   235   240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
                245   250   255
Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly
            260   265   270
Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His
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His His His
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<213> Homo sapiens

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<222> (28)...(897)

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                           Met Lys Tyr Leu Leu Pro Thr Ala Ala
                            1   5

gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag   102
Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln

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 10                  15                  20                  25

ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag      150
Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
                30                  35                  40

atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac      198
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
            45                  50                  55

tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att      246
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
        60                  65                  70

aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag      294
Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys
    75                  80                  85

gac aag gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg      342
Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met
90                  95                  100                 105

caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca      390
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
                110                 115                 120

aga tat tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc      438
Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr
            125                 130                 135

act ctc aca gtc tcc tca gcc aaa aca aca ccc aag ctt ggc ggt gat      486
Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp
        140                 145                 150

atc ttg ctc acc caa act cca gct tct ttg gct gtg tct cta ggg cag      534
Ile Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
    155                 160                 165

agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt      582
Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly
170                 175                 180                 185

gat agt tat ttg aac tgg tac caa cag att cca gga cag cca ccc aaa      630
Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
                190                 195                 200

ctc ctc atc tat gat gca tcc aat cta gtt tct ggg atc cca ccc agg      678
Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg
            205                 210                 215

ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat cct      726
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro
        220                 225                 230

gtg gag aag gtg gat gct gca acc tat cac tgt cag caa agt act gag      774
Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu
    235                 240                 245
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gat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgg gct      822
Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
250                 255                 260                 265

gat gct gcg gcc gct gga tcc gaa caa aag ctg atc tca gaa gaa gac      870
Asp Ala Ala Ala Ala Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp
                270                 275                 280

cta aac tca cat cac cat cac cat cac taaagatct                        906
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<210> 4
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<213> Homo sapiens

<400> 4

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
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            20                  25                  30
Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35                  40                  45
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50                  55                  60
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65                  70                  75                  80
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Asp Lys Ala Thr Leu Thr Thr
                85                  90                  95
Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
            100                 105                 110
Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
        115                 120                 125
Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala
    130                 135                 140
Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Leu Leu Thr Gln Thr Pro
145                 150                 155                 160
Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
                165                 170                 175
Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
            180                 185                 190
Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
        195                 200                 205
Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
    210                 215                 220
Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
225                 230                 235                 240
Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
                245                 250                 255
Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Ala Ala Gly Ser
            260                 265                 270
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His
        275                 280                 285
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290

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gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag 102
Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
10 15 20 25

ctg cag cag tct ggg gct gag ctg gtg agg cct ggg tcc tca gtg aag 150
Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys
30 35 40

E1 att tcc tgc aag gct tct ggc tat gca ttc agt agc tac tgg atg aac 198
Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn
45 50 55

tgg gtg aag cag agg cct gga cag ggt ctt gag tgg att gga cag att 246
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile
60 65 70

tgg cct gga gat ggt gat act aac tac aat gga aag ttc aag ggt aaa 294
Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys
75 80 85

gcc act ctg act gca gac gaa tcc tcc agc aca gcc tac atg caa ctc 342
Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu
90 95 100 105

agc agc cta gca tct gag gac tct gcg gtc tat ttc tgt gca aga cgg 390
Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg
110 115 120

gag act acg acg gta ggc cgt tat tac tat gct atg gac tac tgg ggt 438
Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
125 130 135

caa gga acc tca gtc acc gtc tcc tca gcc aaa aca aca ccc aag ctt 486
Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu
140 145 150

ggc ggt gat atc gtg ctc act cag tct cca gca atc atg tct gca tct 534
Gly Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
155 160 165

cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca agt gta agt 582

```
Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
170                 175                 180                 185

tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc aaa aga tgg      630
Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp
                190                 195                 200

att tat gac aca tcc aaa ctg gct tct gga gtc cct gct cac ttc agg      678
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg
            205                 210                 215

ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc ggc atg gag      726
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu
        220                 225                 230

gct gaa gat gct gcc act tat tac tgc cag cag tgg agt agt aac cca      774
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
    235                 240                 245

ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg gct gat act      822
Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr
250                 255                 260                 265

gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa gac cta aac      870
Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
                270                 275                 280

tca cat cac cat cac cat cac taatctaga                               900
Ser His His His His His His
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E1

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<212> PRT
<213> Homo sapiens

<400> 6

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            20                  25                  30
Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
        35                  40                  45
Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
    50                  55                  60
Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
65                  70                  75                  80
Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
                85                  90                  95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
            100                 105                 110
Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
        115                 120                 125
Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
    130                 135                 140
Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Val Leu Thr
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145                 150                 155                 160
Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
                165                 170                 175
Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
            180                 185                 190
Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu
        195                 200                 205
Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser
    210                 215                 220
Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr
225                 230                 235                 240
Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr
                245                 250                 255
Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln
            260                 265                 270
Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His His His
        275                 280                 285
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<210> 7
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<400> 7
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E1

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<400> 8
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<210> 9
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<212> DNA
<213> Homo sapiens

<400> 9
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<210> 10
<211> 38
<212> DNA
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<400> 10
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<210> 11
<211> 38
<212> DNA
<213> Homo sapiens

<400> 11
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